PAGE: 1

**RAW SEQUENCE LISTING**
**PATENT APPLICATION** *US/08/113,561*

DATE: 09/07/93
TIME: 10:40:48

*INPUT SET: S1441.raw*

```
 1                               SEQUENCE LISTING
 2
 3    (1)    General Information:
 4
 5       (i)  APPLICANTS: Adams, Thomas R. et al.
 6
 7      (ii)  TITLE OF INVENTION: Methods and Compositions for the
 8            Production of Stably Transformed, Fertile, Monocot Plants
 9            and Cells Thereof
10
11     (iii) NUMBER OF SEQUENCES: 13
12
13      (iv) CORRESPONDENCE ADDRESS:
14            (A)  ADDRESSEE: Arnold, White & Durkee
15            (B)  STREET: P.O. BOX 4433
16            (C)  CITY: Houston
17            (D)  STATE: TX
18            (E)  COUNTRY: USA
19            (F)  ZIP: 77210
20
21       (v) COMPUTER READABLE FORM:
22            (A)  MEDIUM TYPE: Floppy disk
23            (B)  COMPUTER: IBM PC compatible
24            (C)  OPERATING SYSTEM: PC-DOS/MS-DOS
25            (D)  SOFTWARE: Patent In Release #1.0, Version #1.25
26
27      (vi) CURRENT APPLICATION DATA:
28            (A)  APPLICATION NUMBER: unknown
29            (B)  FILING DATE: August 25, 1993
30            (C)  CLASSIFICATION: unknown
31
32    (viii) ATTORNEY/AGENT INFORMATION:
33            (A)  NAME: Parker, David L.
34            (B)  REGISTRATION NUMBER: 32,165
35            (C)  REFERENCE/DOCKET NUMBER: DEKA:055/PAR
36
37      (ix) TELECOMMUNICATION INFORMATION:
38            (A)  TELEPHONE: 512-320-7200
39            (B)  TELEFAX: 512-474-7577
40            (C)  TELEX: NOT APPLICABLE
41
42
43    (2) INFORMATION FOR SEQ ID NO:1:
44
45       (i) SEQUENCE CHARACTERISTICS:
46            (A)   LENGTH: 15 amino acid residues
47            (B)   TYPE: amino acid
48            (C)   STRANDEDNESS: single
49            (D)   TOPOLOGY: linear
50
51      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
```

PAGE: 2

**RAW SEQUENCE LISTING**
PATENT APPLICATION  *US/08/113,561*

DATE: 09/07/93
TIME: 10:40:49

*INPUT SET: S1441.raw*

```
52
53    Met Ala Thr Val Pro Glu Leu Asn Cys Glu Met Pro Pro Ser Asp
54     1               5                10                15
55
56
57    (2) INFORMATION FOR SEQ ID NO:2:
58
59        (i) SEQUENCE CHARACTERISTICS:
60            (A) LENGTH: 35 base pairs
61            (B) TYPE: nucleic acid
62            (C) STRANDEDNESS: single
63            (D) TOPOLOGY: linear
64
65       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
66
67    GAGGATCCGT CGACATGGTA AGCTTAGCGG GCCCC                         35
68
69
70    (2)    INFORMATION FOR SEQ ID NO:3:
71
72        (i) SEQUENCE CHARACTERISTICS:
73            (A) LENGTH: 29 base pairs
74            (B) TYPE: nucleic acid
75            (C) STRANDEDNESS: single
76            (D) TOPOLOGY: linear
77
78       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
79
80    GATCCGTCGA CCATGGCGCT TCAAGCTTC
81        29
82
83
84    (2) INFORMATION FOR SEQ ID NO:4:
85
86        (i) SEQUENCE CHARACTERISTICS:
87            (A) LENGTH: 29 base pairs
88            (B) TYPE: nucleic acid
89            (C) STRANDEDNESS: single
90            (D) TOPOLOGY: linear
91
92       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
93
94    GCAGCTGGTA CCGCGAAGTT CGAAGGGCT
95        29
96
97
98    (2) INFORMATION FOR SEQ ID NO:5:
99
100       (i) SEQUENCE CHARACTERISTICS:
101           (A) LENGTH: 49 base pairs
102           (B) TYPE: nucleic acid
```

```
103                     (C) STRANDEDNESS: single
104                     (D) TOPOLOGY: linear
105
106          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
107
108    CTAGACAACA AAGCAGCAAC CATGGCCAGC ATGCAAGGCC TCATGCATC
109                                                              49
110
111
112    (2) INFORMATION FOR SEQ ID NO:6:
113
114          (i) SEQUENCE CHARACTERISTICS:
115                     (A) LENGTH: 49 base pairs
116                     (B) TYPE: nucleic acid
117                     (C) STRANDEDNESS: single
118                     (D) TOPOLOGY: linear
119
120          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
121
122    CCGGGATGCA TGAGGCCTTG CATGCTGGCC ATGGTTGCTG CTTTGTTGT
123         49
124
125
126    (2) INFORMATION FOR SEQ ID NO:7:
127
128          (i) SEQUENCE CHARACTERISTICS:
129                     (A) LENGTH: 11 amino acid residues
130                     (B) TYPE: amino acid
131                     (C) STRANDEDNESS: single
132                     (D) TOPOLOGY: linear
133
134          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
135
136    Met Ala Ser Met Gln Gly Leu Met His Pro Gly
137     1               5                   10
138
139
140    (2) INFORMATION FOR SEQ ID NO:8:
141
142          (i) SEQUENCE CHARACTERISTICS:
143                     (A) LENGTH: 6 amino acid residues
144                     (B) TYPE: amino acid
145                     (C) STRANDEDNESS: single
146                     (D) TOPOLOGY: linear
147
148          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
149
150    Val Lys Cys Met Gln Val
151     1               5
152
153
```

```
154    (2)  INFORMATION FOR SEQ ID NO:9:
155
156         (i)  SEQUENCE CHARACTERISTICS:
157              (A)  LENGTH: 18 base pairs
158              (B)  TYPE: nucleic acid
159              (C)  STRANDEDNESS: single
160              (D)  TOPOLOGY: linear
161
162        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:9:
163
164    AAGUGAAGUG AAGUGAAG
165         18
166
167
168    (2)  INFORMATION FOR SEQ ID NO:10:
169
170         (i)  SEQUENCE CHARACTERISTICS:
171              (A)  LENGTH: 1845 base pairs
172              (B)  TYPE: nucleic acid
173              (C)  STRANDEDNESS: single
174              (D)  TOPOLOGY: linear
175
176        (ii)  MOLECULE TYPE: DNA (genomic)
177
178        (ix)  FEATURE:
179              (A)  NAME/KEY: CDS
180              (B)  LOCATION: 1..1839
181
182        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:10:
183
184    ATG GAT AAC AAT CCG AAC ATC AAT GAA TGC ATT CCT TAC AAT TGC CTC
185         48
186    Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu
187     1               5                  10                  15
188
189    AGC AAC CCT GAA GTG GAA GTG CTG GGT GGC GAA CGC ATC GAA ACC GGT
190         96
191    Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly
192                 20              25                  30
193
194    TAC ACC CCA ATC GAT ATT TCC CTG TCC CTG ACC CAA TTT CTG CTG AGC
195         144
196    Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser
197              35              40                  45
198
199    GAA TTT GTG CCC GGT GCT GGC TTT GTG CTG GGC CTG GTG GAT ATC ATC
200         192
201    Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
202          50              55                  60
203
204    TGG GGC ATT TTT GGT CCC TCC CAA TGG GAC GCC TTT CTG GTG CAA ATT
```

PAGE: 5

**RAW SEQUENCE LISTING**
**PATENT APPLICATION** *US/08/113,561*

DATE: 09/07/93
TIME: 10:40:54

*INPUT SET: S1441.raw*

```
205         240
206   Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile
207    65                   70              75                  80
208
209   GAA CAG CTG ATT AAC CAA CGC ATC GAA GAA TTC GCT AGG AAC CAA GCC
210    288
211   Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
212                   85                  90                  95
213
214   ATT TCC CGC CTG GAA GGC CTG AGC AAT CTG TAC CAA ATT TAC GCC GAA
215    336
216   Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
217              100             105             110
218
219   TCC TTT CGC GAG TGG GAA GCC GAT CCT ACC AAT CCA GCC CTG CGC GAA
220    384
221   Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu
222          115             120             125
223
224   GAG ATG CGC ATT CAA TTC AAT GAC ATG AAC AGC GCC CTG ACC ACC GCT
225    432
226   Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
227       130             135             140
228
229   ATT CCT CTG TTT GCC GTG CAA AAT TAC CAA GTG CCT CTG CTG TCC GTG
230    480
231   Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
232   145             150             155             160
233
234   TAC GTG CAA GCT GCC AAT CTG CAT CTG TCC GTG CTG CGC GAT GTG TCC
235    528
236   Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser
237                   165             170             175
238
239   GTG TTT GGC CAA AGG TGG GGC TTT GAT GCC GCC ACC ATC AAT AGC CGC
240    576
241   Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
242              180             185             190
243
244   TAC AAT GAT CTG ACC AGG CTG ATT GGC AAC TAC ACC GAT TAC GCT GTG
245    624
246   Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
247              195             200             205
248
249   CGC TGG TAC AAT ACC GGC CTG GAA CGC GTG TGG GGC CCA GAT TCC CGC
250    672
251   Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
252       210             215             220
253
254   GAT TGG GTG AGG TAC AAT CAA TTT CGC CGC GAA CTG ACC CTG ACC GTG
255    720
```

```
256    Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
257    225                 230             235                 240
258
259    CTC GAT ATC GTG GCT CTG TTC CCA AAT TAC GAT AGC CGC CGC TAC CCA
260        768
261    Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro
262                    245             250                 255
263
264    ATT CGA ACC GTG TCC CAA CTG ACC CGC GAA ATT TAC ACC AAC CCA GTG
265        816
266    Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
267                260             265                 270
268
269    CTG GAA AAT TTT GAT GGT AGC TTT CGC GGC TCC GCT CAG GGC ATC GAA
270        864
271    Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
272                275             280                 285
273
274    CGC AGC ATT AGG AGC CCA CAT CTG ATG GAT ATC CTG AAC AGC ATC ACC
275        912
276    Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
277        290             295                 300
278
279    ATC TAC ACC GAT GCT CAT AGG GGT TAC TAC TAC TGG TCC GGC CAT CAA
280        960
281    Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Tyr Trp Ser Gly His Gln
282    305                 310                 315                 320
283
284    ATC ATG GCT TCC CCT GTG GGC TTT TCC GGG CCA GAA TTC ACC TTT CCA
285        1008
286    Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
287                    325             330                 335
288
289    CTG TAC GGC ACG ATG GGC AAT GCC GCT CCA CAA CAA CGC ATT GTG GCT
290        1056
291    Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
292                340             345                 350
293
294    CAA CTG GGT CAG GGC GTG TAC CGC ACC CTG TCC TCC ACC CTG TAC CGC
295        1104
296    Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
297                355             360                 365
298
299    CGC CCT TTT AAT ATC GGC ATC AAC AAC CAG CAA CTG TCC GTG CTG GAC
300        1152
301    Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
302        370             375                 380
303
304    GGC ACC GAA TTT GCT TAC GGC ACC TCC TCC AAT CTG CCA TCC GCT GTA
305        1200
306    Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
```

PAGE: 7

**RAW SEQUENCE LISTING**
**PATENT APPLICATION** *US/08/113,561*

DATE: 09/07/93
TIME: 10:40:57

*INPUT SET: S1441.raw*

```
307   385                    390                    395                    400

308

309   TAC CGC AAG AGC GGC ACC GTG GAT TCC CTG GAT GAA ATC CCA CCA CAG
310      1248
311   Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
312             405             410             415

313

314   AAT AAC AAC GTG CCA CCT AGG CAA GGC TTT AGC CAT CGC CTG AGC CAT
315      1296
316   Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
317             420             425             430

318

319   GTG TCC ATG TTT CGC TCC GGC TTT AGC AAT AGC AGC GTG AGC ATC ATC
320      1344
321   Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
322             435             440             445

323

324   CGC GCT CCT ATG TTC TCC TGG ATC CAT CGC AGC GCT GAA TTT AAC AAC
325      1392
326   Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn
327      450             455             460

328

329   ATC ATT GCC TCC GAT AGC ATT ACC CAA ATC CCT GCC GTG AAG GGC AAC
330      1440
331   Ile Ile Ala Ser Asp Ser Ile Thr Gln Ile Pro Ala Val Lys Gly Asn
332   465             470             475             480

333

334   TTT CTG TTT AAT GGT TCC GTG ATT TCC GGC CCA GGC TTT ACC GGT GGC
335      1488
336   Phe Leu Phe Asn Gly Ser Val Ile Ser Gly Pro Gly Phe Thr Gly Gly
337             485             490             495

338

339   GAC CTG GTG CGC CTG AAT AGC AGC GGC AAT AAC ATT CAG AAT CGC GGC
340      1536
341   Asp Leu Val Arg Leu Asn Ser Ser Gly Asn Asn Ile Gln Asn Arg Gly
342             500             505             510

343

344   TAC ATT GAA GTG CCA ATT CAC TTC CCA TCC ACC TCC ACC CGC TAC CGC
345      1584
346   Tyr Ile Glu Val Pro Ile His Phe Pro Ser Thr Ser Thr Arg Tyr Arg
347             515             520             525

348

349   GTG CGC GTG CGC TAC GCT TCC GTG ACC CCA ATT CAC CTC AAC GTT AAC
350      1632
351   Val Arg Val Arg Tyr Ala Ser Val Thr Pro Ile His Leu Asn Val Asn
352             530             535             540

353

354   TGG GGC AAT TCC TCC ATT TTT TCC AAT ACC GTG CCA GCT ACC GCT ACC
355      1680
356   Trp Gly Asn Ser Ser Ile Phe Ser Asn Thr Val Pro Ala Thr Ala Thr
357   545             550             555             560
```

PAGE: 8

RAW SEQUENCE LISTING
PATENT APPLICATION  *US/08/113,561*

DATE: 09/07/93
TIME: 10:41:13

*INPUT SET: S1441.raw*

```
358
359      TCC CTG GAT AAT CTG CAA TCC AGC GAT TTT GGT TAC TTT GAA AGC GCC
360         1728
361      Ser Leu Asp Asn Leu Gln Ser Ser Asp Phe Gly Tyr Phe Glu Ser Ala
362                      565             570             575
363
364      AAT GCT TTT ACC TCC TCC CTG GGT AAT ATC GTG GGT GTG CGC AAT TTT
365         1776
366      Asn Ala Phe Thr Ser Ser Leu Gly Asn Ile Val Gly Val Arg Asn Phe
367                  580             585             590
368
369      AGC GGC ACC GCC GGC GTG ATC ATC GAC CGC TTT GAA TTT ATT CCA GTG
370         1824
371      Ser Gly Thr Ala Gly Val Ile Ile Asp Arg Phe Glu Phe Ile Pro Val
372              595             600             605
373
374      ACC GCC ACC CTC GAG TAGGTA
375         1845
376      Thr Ala Thr Leu Glu
377         610
378
379      (2) INFORMATION FOR SEQ ID NO:11:
380
381            (i) SEQUENCE CHARACTERISTICS:
382                (A) LENGTH: 613 amino acids
383                (B) TYPE: amino acid
384                (D) TOPOLOGY: linear
385
386           (ii) MOLECULE TYPE: protein
387
388           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
389
390      Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu
391       1               5              10               15
392
393      Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly
394                  20              25               30
395
396      Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser
397              35              40               45
398
399      Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
400          50              55               60
401
402      Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile
403       65              70               75               80
404
405      Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
406                  85              90               95
407
408      Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
```

```
409                 100                 105                 110
410
411     Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu
412             115             120             125
413
414     Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
415          130             135             140
416
417     Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
418     145             150             155             160
419
420     Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser
421             165             170             175
422
423     Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
424             180             185             190
425
426     Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
427             195             200             205
428
429     Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
430             210             215             220
431
432     Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
433     225             230             235             240
434
435     Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro
436             245             250             255
437
438     Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
439             260             265             270
440
441     Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
442             275             280             285
443
444     Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
445             290             295             300
446
447     Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Tyr Trp Ser Gly His Gln
448     305             310             315             320
449
450     Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
451             325             330             335
452
453     Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
454             340             345             350
455
456     Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
457             355             360             365
458
459     Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
```

*INPUT SET: S1441.raw*

```
460         370                    375                    380
461
462    Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
463    385                 390                 395                 400
464
465    Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
466                405                 410                 415
467
468    Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
469                420                 425                 430
470
471    Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
472            435                 440                 445
473
474    Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn
475        450                 455                 460
476
477    Ile Ile Ala Ser Asp Ser Ile Thr Gln Ile Pro Ala Val Lys Gly Asn
478    465                 470                 475                 480
479
480    Phe Leu Phe Asn Gly Ser Val Ile Ser Gly Pro Gly Phe Thr Gly Gly
481                485                 490                 495
482
483    Asp Leu Val Arg Leu Asn Ser Ser Gly Asn Asn Ile Gln Asn Arg Gly
484            500                 505                 510
485
486    Tyr Ile Glu Val Pro Ile His Phe Pro Ser Thr Ser Thr Arg Tyr Arg
487            515                 520                 525
488
489    Val Arg Val Arg Tyr Ala Ser Val Thr Pro Ile His Leu Asn Val Asn
490        530                 535                 540
491
492    Trp Gly Asn Ser Ser Ile Phe Ser Asn Thr Val Pro Ala Thr Ala Thr
493    545                 550                 555                 560
494
495    Ser Leu Asp Asn Leu Gln Ser Ser Asp Phe Gly Tyr Phe Glu Ser Ala
496                565                 570                 575
497
498    Asn Ala Phe Thr Ser Ser Leu Gly Asn Ile Val Gly Val Arg Asn Phe
499                580                 585                 590
500
501    Ser Gly Thr Ala Gly Val Ile Ile Asp Arg Phe Glu Phe Ile Pro Val
502            595                 600                 605
503
504    Thr Ala Thr Leu Glu
505        610
506
507    (2) INFORMATION FOR SEQ ID NO:12:
508
509        (i) SEQUENCE CHARACTERISTICS:
510            (A) LENGTH: 1848 base pairs
```

*INPUT SET: S1441.raw*

```
511              (B)  TYPE: nucleic acid
512              (C)  STRANDEDNESS: single
513              (D)  TOPOLOGY: linear
514
515        (ii)  MOLECULE TYPE: DNA (genomic)
516
517        (ix)  FEATURE:
518              (A)  NAME/KEY: CDS
519              (B)  LOCATION: 1..1842
520
521        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:12:
522
523   ATG GAT AAC AAT CCG AAC ATC AAT GAA TGC ATT CCT TAC AAT TGC CTC
524       48
525   Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu
526    1               5                  10                  15
527
528   AGC AAC CCT GAA GTG GAA GTG CTG GGT GGC GAA CGC ATC GAA ACC GGT
529       96
530   Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly
531              20                  25                  30
532
533   TAC ACC CCA ATC GAT ATT TCC CTG TCC CTG ACC CAA TTT CTG CTG AGC
534       144
535   Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser
536              35                  40                  45
537
538   GAA TTT GTG CCC GGT GCT GGC TTT GTG CTG GGC CTG GTG GAT ATC ATC
539       192
540   Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
541          50                  55                  60
542
543   TGG GGC ATT TTT GGT CCC TCC CAA TGG GAC GCC TTT CTG GTG CAA ATT
544       240
545   Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile
546    65                  70                  75                  80
547
548   GAA CAG CTG ATT AAC CAA CGC ATC GAA GAA TTC GCT AGG AAC CAA GCC
549       288
550   Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
551                  85                  90                  95
552
553   ATT TCC CGC CTG GAA GGC CTG AGC AAT CTG TAC CAA ATT TAC GCC GAA
554       336
555   Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
556              100                 105                 110
557
558   TCC TTT CGC GAG TGG GAA GCC GAT CCT ACC AAT CCA GCC CTG CGC GAA
559       384
560   Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu
561              115                 120                 125
```

```
562
563    GAG ATG CGC ATT CAA TTC AAT GAC ATG AAC AGC GCC CTG ACC ACC GCT
564        432
565    Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
566        130                 135             140
567
568    ATT CCT CTG TTT GCC GTG CAA AAT TAC CAA GTG CCT CTG CTG TCC GTG
569        480
570    Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
571    145                 150             155             160
572
573    TAC GTG CAA GCT GCC AAT CTG CAT CTG TCC GTG CTG CGC GAT GTG TCC
574        528
575    Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser
576                165             170             175
577
578    GTG TTT GGC CAA AGG TGG GGC TTT GAT GCC GCC ACC ATC AAT AGC CGC
579        576
580    Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
581                180             185             190
582
583    TAC AAT GAT CTG ACC AGG CTG ATT GGC AAC TAC ACC GAT TAC GCT GTG
584        624
585    Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
586                195             200             205
587
588    CGC TGG TAC AAT ACC GGC CTG GAA CGC GTG TGG GGC CCA GAT TCC CGC
589        672
590    Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
591        210             215             220
592
593    GAT TGG GTG AGG TAC AAT CAA TTT CGC CGC GAA CTG ACC CTG ACC GTG
594        720
595    Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
596    225             230             235             240
597
598    CTC GAT ATC GTG GCT CTG TTC CCA AAT TAC GAT AGC CGC CGC TAC CCA
599        768
600    Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro
601                245             250             255
602
603    ATT CGA ACC GTG TCC CAA CTG ACC CGC GAA ATT TAC ACC AAC CCA GTG
604        816
605    Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
606                260             265             270
607
608    CTG GAA AAT TTT GAT GGT AGC TTT CGC GGC TCC GCT CAG GGC ATC GAA
609        864
610    Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
611                275             280             285
612
```

```
613   CGC AGC ATT AGG AGC CCA CAT CTG ATG GAT ATC CTG AAC AGC ATC ACC
614       912
615   Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
616       290               295               300
617
618   ATC TAC ACC GAT GCT CAT AGG GGT TAC TAC TAC TGG TCC GGC CAT CAA
619       960
620   Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Tyr Trp Ser Gly His Gln
621   305               310               315               320
622
623   ATC ATG GCT TCC CCT GTG GGC TTT TCC GGG CCA GAA TTC ACC TTT CCA
624       1008
625   Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
626               325               330               335
627
628   CTG TAC GGC ACG ATG GGC AAT GCC GCT CCA CAA CAA CGC ATT GTG GCT
629       1056
630   Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
631               340               345               350
632
633   CAA CTG GGT CAG GGC GTG TAC CGC ACC CTG TCC TCC ACC CTG TAC CGC
634       1104
635   Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
636               355               360               365
637
638   CGC CCT TTT AAT ATC GGC ATC AAC AAC CAG CAA CTG TCC GTG CTG GAC
639       1152
640   Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
641       370               375               380
642
643   GGC ACC GAA TTT GCT TAC GGC ACC TCC TCC AAT CTG CCA TCC GCT GTA
644       1200
645   Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
646   385               390               395               400
647
648   TAC CGC AAG AGC GGC ACC GTG GAT TCC CTG GAT GAA ATC CCA CCA CAG
649       1248
650   Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
651               405               410               415
652
653   AAT AAC AAC GTG CCA CCT AGG CAA GGC TTT AGC CAT CGC CTG AGC CAT
654       1296
655   Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
656               420               425               430
657
658   GTG TCC ATG TTT CGC TCC GGC TTT AGC AAT AGC AGC GTG AGC ATC ATC
659       1344
660   Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
661               435               440               445
662
663   CGC GCT CCT ATG TTC TCC TGG ATC CAC CGC TCC GCT GAG TTC AAC AAC
```

```
664      1392
665    Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn
666        450                 455             460
667
668    ATC ATC CCG TCC TCC CAA ATC ACC CAA ATC CCG CTC ACC AAG TCC ACG
669      1440
670    Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr
671    465             470             475                 480
672
673    AAC CTC GGC TCC GGC ACG TCC GTC GTC AAG GGC CCG GGC TTC ACC GGC
674      1488
675    Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly
676                485             490                 495
677
678    GGC GAC ATC CTC CGC CGC ACG TCC CCG GGC CAG ATC TCC ACC CTC CGC
679      1536
680    Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg
681            500             505                 510
682
683    GTC AAC ATC ACG GCT CCG CTG AGC CAG CGC TAC AGG GTG CGC ATC AGA
684      1584
685    Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg
686            515             520                 525
687
688    TAC GCT AGC ACG ACC AAC CTG CAA TTC CAC ACG TCC ATC GAC GGC AGA
689      1632
690    Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg
691        530             535                 540
692
693    CCG ATC AAC CAG GGC AAC TTC AGC GCG ACG ATG AGC TCC GGG TCC AAC
694      1680
695    Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn
696    545             550             555                 560
697
698    CTC CAG TCC GGC TCC TTC CGC ACG GTC GGT TTC ACC ACG CCG TTC AAC
699      1728
700    Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn
701                565             570                 575
702
703    TTC TCC AAC GGC TCC TCC GTC TTC ACG CTC TCC GCT CAC GTC TTC AAC
704      1776
705    Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn
706                580             585                 590
707
708    TCC GGC AAC GAG GTG TAC ATC GAC CGC ATC GAG TTC GTC CCG GCC GAG
709      1824
710    Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu
711                595             600                 605
712
713    GTC ACC TTC GAG CTC GAG TAGGTA
714      1848
```

PAGE: 15

**RAW SEQUENCE LISTING**
**PATENT APPLICATION** *US/08/113,561*

DATE: 09/07/93
TIME: 10:42:00

*INPUT SET: S1441.raw*

```
715    Val Thr Phe Glu Leu Glu
716       610
717
718
719    (2) INFORMATION FOR SEQ ID NO:13:
720
721         (i) SEQUENCE CHARACTERISTICS:
722              (A) LENGTH: 614 amino acids
723              (B) TYPE: amino acid
724              (D) TOPOLOGY: linear
725
726        (ii) MOLECULE TYPE: protein
727
728        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
729
730    Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu
731     1               5               10              15
732
733    Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly
734           20              25              30
735
736    Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser
737           35              40              45
738
739    Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
740         50              55              60
741
742    Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile
743     65              70              75              80
744
745    Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
746               85              90              95
747
748    Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
749           100             105             110
750
751    Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu
752           115             120             125
753
754    Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
755         130             135             140
756
757    Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
758    145             150             155             160
759
760    Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser
761               165             170             175
762
763    Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
764               180             185             190
765
```

```
766    Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
767        195                 200                 205
768
769    Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
770        210                 215                 220
771
772    Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
773    225                 230                 235                 240
774
775    Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro
776                245                 250                 255
777
778    Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
779                260                 265                 270
780
781    Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
782        275                 280                 285
783
784    Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
785        290                 295                 300
786
787    Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Tyr Trp Ser Gly His Gln
788    305                 310                 315                 320
789
790    Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
791                325                 330                 335
792
793    Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
794                340                 345                 350
795
796    Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
797        355                 360                 365
798
799    Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
800        370                 375                 380
801
802    Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
803    385                 390                 395                 400
804
805    Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
806                405                 410                 415
807
808    Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
809                420                 425                 430
810
811    Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
812        435                 440                 445
813
814    Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn
815        450                 455                 460
816
```

**RAW SEQUENCE LISTING**
**PATENT APPLICATION** *US/08/113,561*

*INPUT SET: S1441.raw*

```
817   Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr
818   465             470             475                 480
819
820   Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly
821               485             490                 495
822
823   Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg
824           500             505                 510
825
826   Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg
827       515             520             525
828
829   Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg
830       530             535             540
831
832   Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn
833   545             550             555                 560
834
835   Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn
836               565             570                 575
837
838   Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn
839               580             585                 590
840
841   Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu
842               595             600                 605
843
844   Val Thr Phe Glu Leu Glu
845       610
846
```

# SEQUENCE VERIFICATION REPORT
## PATENT APPLICATION  *US/08/113,561*

*INPUT SET: S1441.raw*

| Line | Error | Original Text |
|------|-------|---------------|
| 28 | Wrong application Serial Number | (A) APPLICATION NUMBER: unknown |
| 29 | Wrong Filing Date | (B) FILING DATE: August 25, 1993 |
| 30 | Wrong Classification | (C) CLASSIFICATION: unknown |
| 78 | Entered (29) and Calc. Seq. Length (0) differ | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3: |
| 92 | Entered (29) and Calc. Seq. Length (0) differ | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4: |
| 106 | Entered (49) and Calc. Seq. Length (0) differ | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5: |
| 120 | Entered (49) and Calc. Seq. Length (0) differ | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6: |
| 162 | Entered (18) and Calc. Seq. Length (0) differ | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9: |
| 182 | Entered (1845) and Calc. Seq. Length (0) differ | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10: |
| 521 | Entered (1848) and Calc. Seq. Length (0) differ | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12: |

# SEQUENCE MISSING ITEM REPORT
## PATENT APPLICATION US/08/113,561

INPUT SET: S1441.raw

APPLICATION NUMBER
FILING DATE
PRIOR APPLICATION DATA

**SEQUENCE CORRECTION REPORT**
**PATENT APPLICATION  *US/08/113,561***

*INPUT SET: S1441.raw*

| Line | Original Text | Corrected Text |
|---|---|---|
| 5 | (i) APPLICANTS: Adams, Thomas R. et al. | (i) APPLICANT: Adams, Thomas R. et al. |